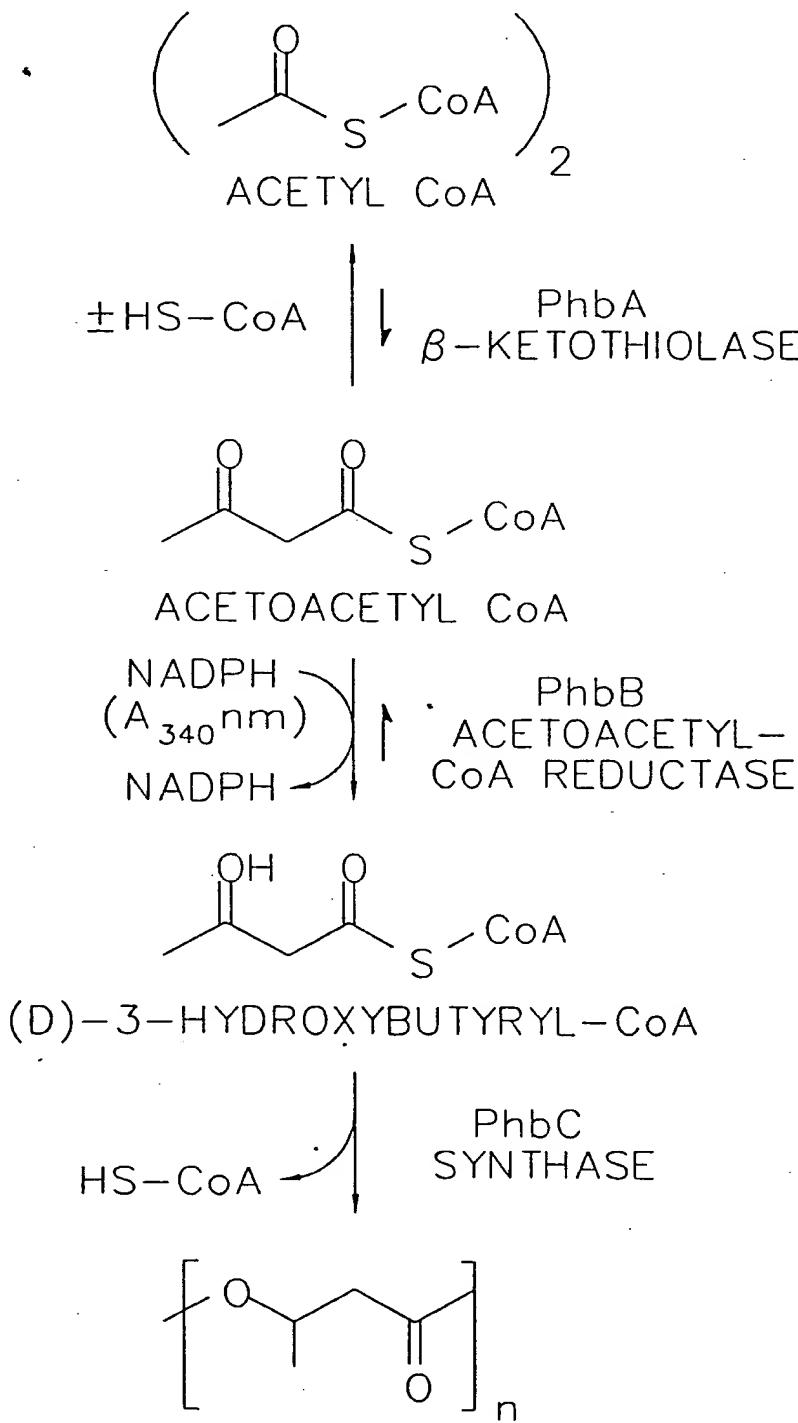


APPROVED	O.G. FIG.
BY	CLASS 278
DRAFTSMAN	800

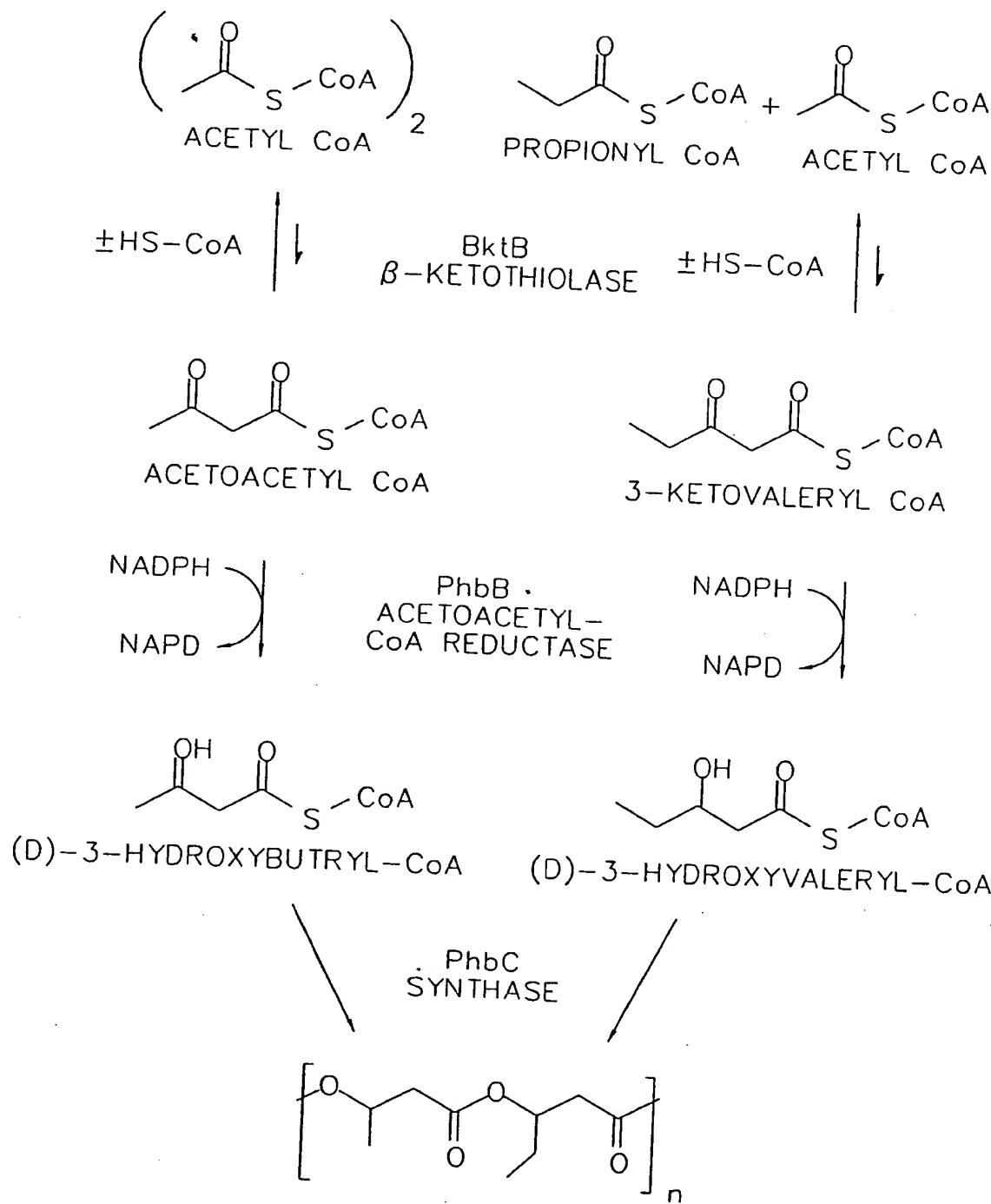
119

FIG. 1



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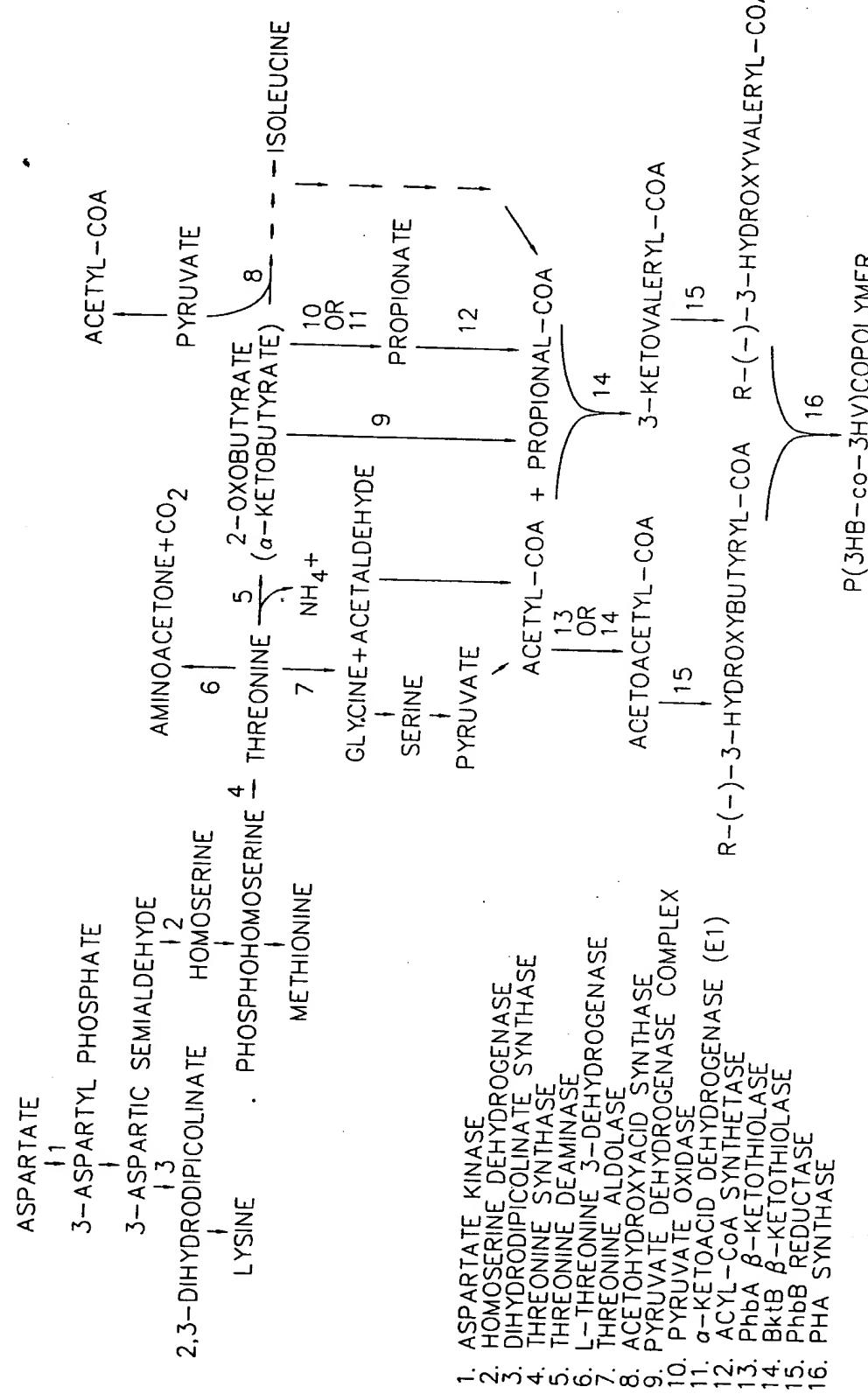
FIG. 2



APPROVED	O. G. FIG.
BY	CLASS / SUBCLASS
DRAFTSMAN	

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FIG. 3



APPROVED BY	Q.G. FIG.	
DRAFTSMAN	CLASS	SUBCLASS

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FIG. 4

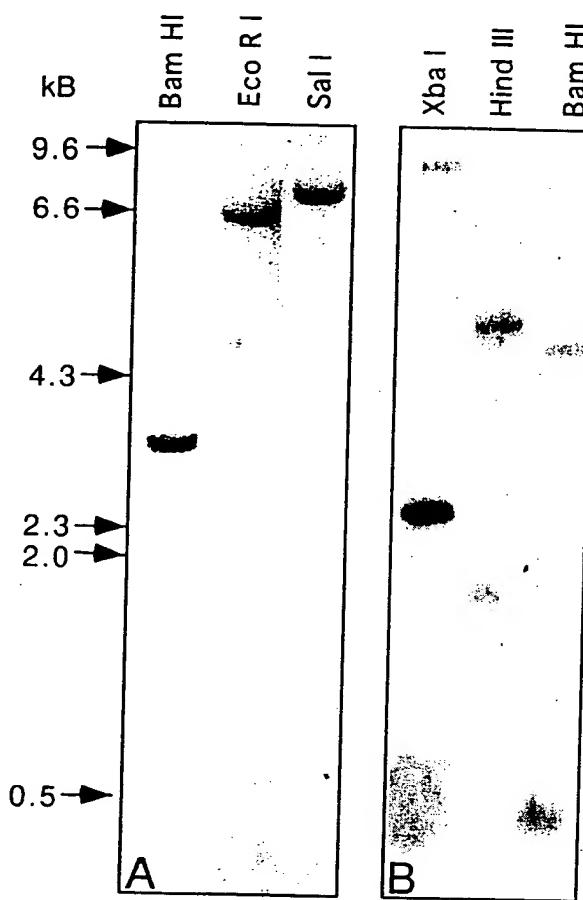
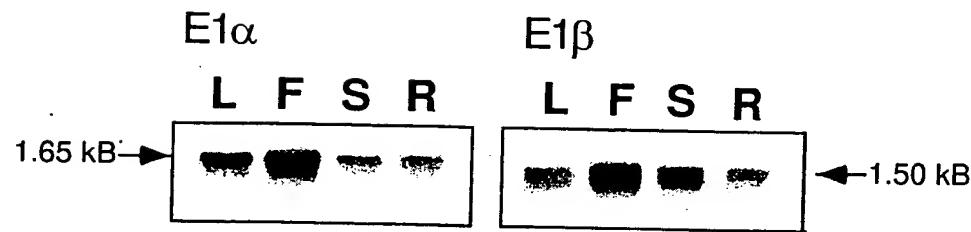


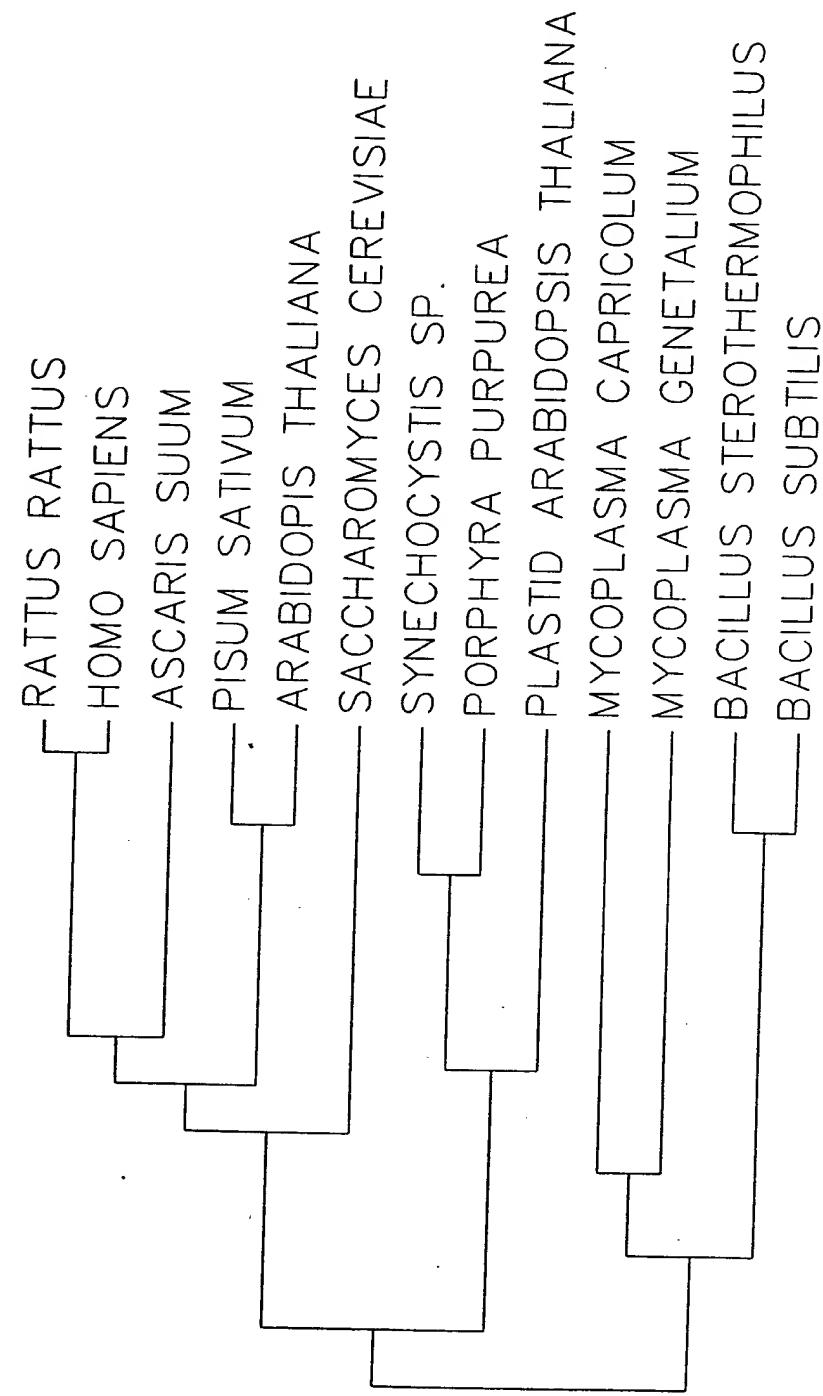
FIG. 5



APPROVED	O. G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

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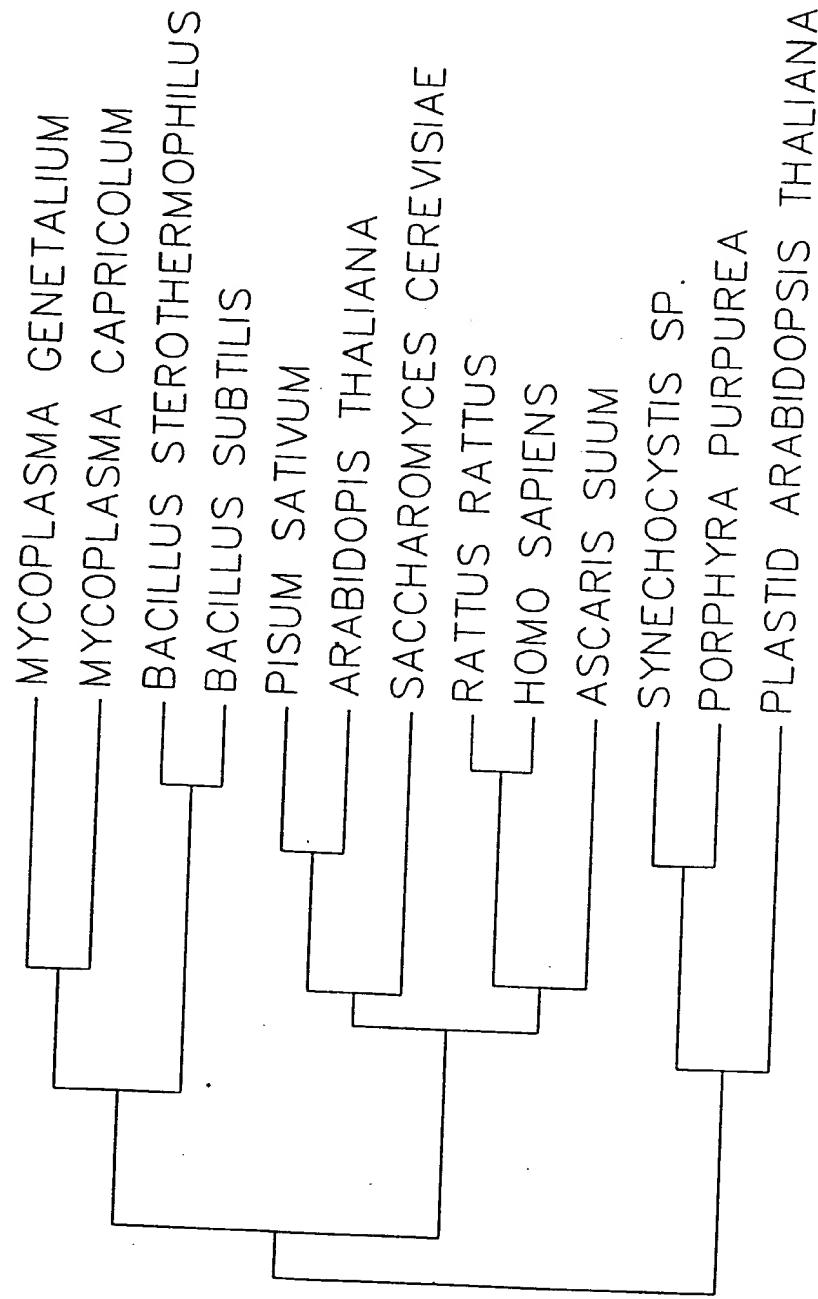
FIG. 6A



APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

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FIG. 6B

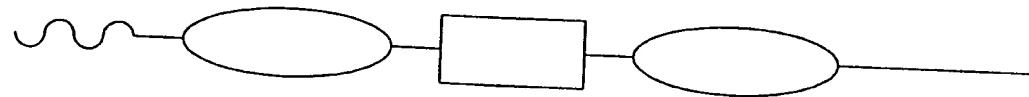


APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

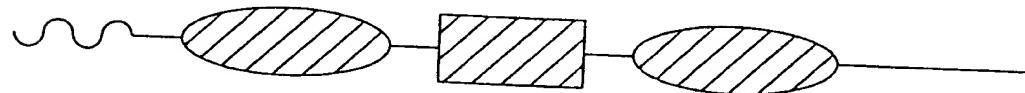
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FIG. 7A

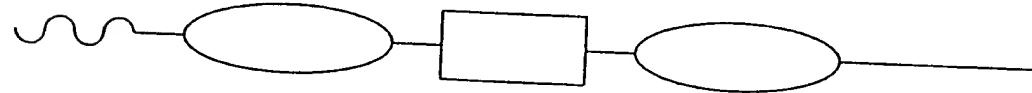
BRANCHED-CHAIN E1 α



PLASTID E1 α



PLASTID TARGETED BRANCHED-CHAIN E1 α CHIMERA



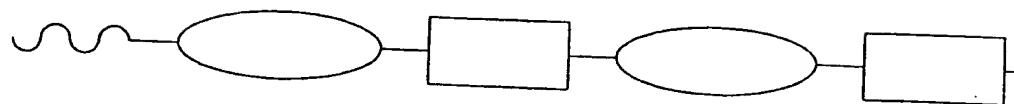
CONSTRUCT 1: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF E1 α TO THE BRANCHED-CHAIN E1 α . THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1 α CHIMERA.

APPROVED BY DRAFTSMAN	O.G. FIG. CLASS	SUBCLASS
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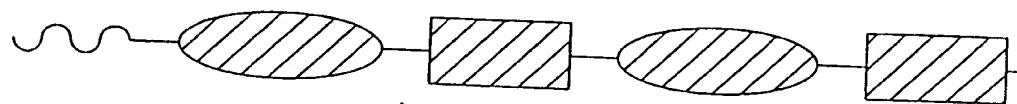
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FIG. 7B

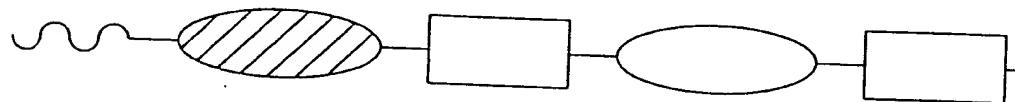
BRANCHED-CHAIN E1 β



PLASTID E1 β



PLASTID TARGETED BRANCHED-CHAIN E1 β CHIMERA



CONSTRUCT 2: REPLACE THE N-TERMINUS OF THE BRANCHED-CHAIN E1 β (INCLUDING THE E2 BINDING DOMAIN) WITH THE N-TERMINUS OF THE PLASTID E1 β (INCLUDING THE CHLOROPLAST TARGETING PEPTIDE AND THE PLASTID E2 BINDING DOMAIN). THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1 β CHIMERA.

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 7C

BRANCHED-CHAIN E2



PLASTID E2



PLASTID TARGETED BRANCHED-CHAIN E2

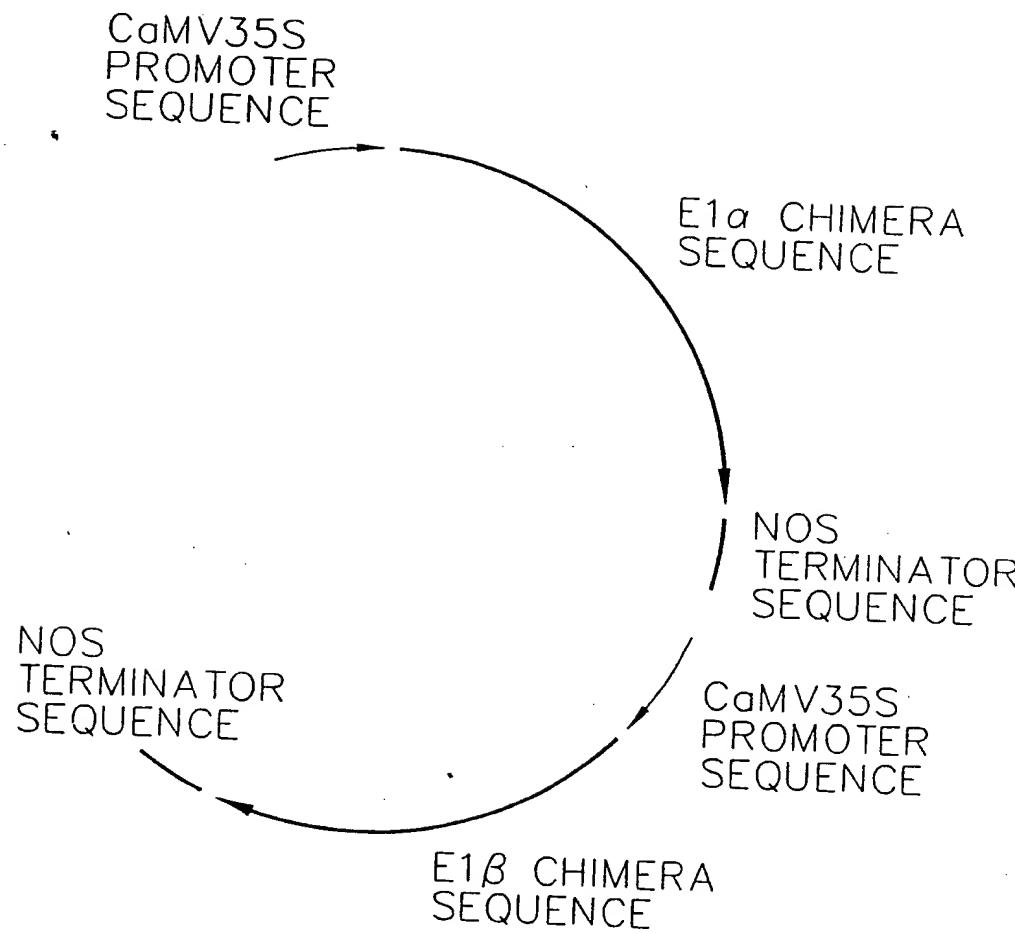


CONSTRUCT 3: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID E2 TO THE MATURE PORTION OF THE BRANCHED-CHAIN E2, TO CREATE A PLASTID TARGETED BRANCHED-CHAIN E2 CHIMERA.

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

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FIG. 7D



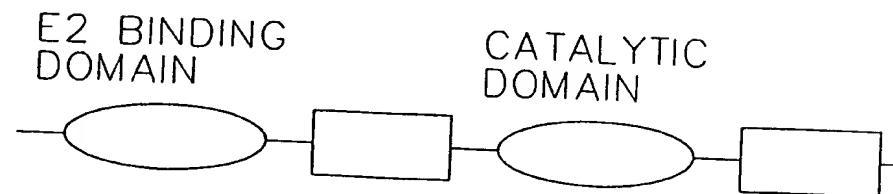
CONSTRUCT 4: MEGA PLASMID CODING FOR BOTH CHIMERIC (PLASTID TARGETED BRANCHED-CHAIN) SUBUNITS IF THE PDH. ATTACH THE E1 α CHIMERIC SEQUENCE TO THE E1 β CHIMERIC SEQUENCE WITH TRANSCRIPTION TERMINATOR AND PROMOTER SEQUENCES BETWEEN THE TWO.

APPROVED	O. G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

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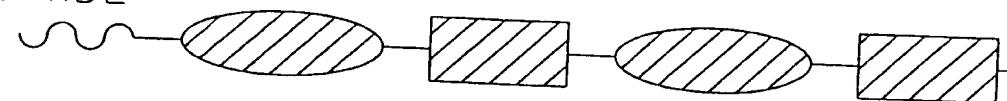
FIG. 7E

BRANCHED-CHAIN E1 β

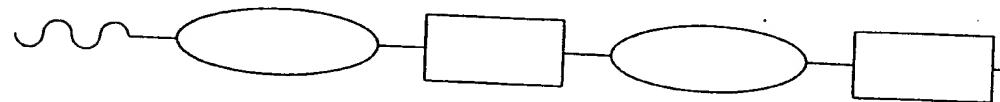


CHLOROPLAST TARGETING PEPTIDE

PLASTID E16



PLASTID TARGETED BRANCHED- CHAIN E1 β CHIMERA



CONSTRUCT 5: ATTACH THE CHLOROPLAST TARGETING PEPTIDE OF THE PLASTID E1 β TO THE MATURE PORTION OF THE BRANCHED-CHAIN E1 β . THIS CREATES A PLASTID TARGETED BRANCHED-CHAIN E1 β CHIMERA.

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APPROVED BY DRAFTSMAN	O.G. FIG. CLASS SUBCLASS
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FIG. 8A

Plastid A.t.	MATAFAPTKLTATVPLHGSHENRLLLPIRLAPPSSFLGSTRSLSLRRLNH	50
<i>P.purpurea</i>	-----	
<i>A.thaliana</i>	-----MALSRLSSRSNIITRPFSAAFSRLIS	26
<i>H.sapiens</i> II	-----MRKMLAAVSRLVLSGASQKPASRVLVAS	27
<i>S.cerevisiae</i>	---MLAASFKRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTTDKKAPEDI	47
<i>A.suum</i> I	-----MIFVFANIFKVPTVSPSVM AISV	23
<i>M.capricolum</i>	-----MTYL	4
<i>B.subtilis</i>	-----MGVKTFQFPFAEQL	14
Consensus	-----	50

Motif 1

SNATRRSPVVSQEVVKEKQSTNNNTSLITKEEGLELYEDMILGRSFEDM	100
-----MSYPKKVELPLTCNCQINLTKHKLVLYEDMLLGRNFEDM	40
TDTTPITIETSLPFTAHLCDPPSRSESSSQELLD-FFRTMALMRRMEIA	75
RNFANDATFEIKKCDLHRLEEGPPVTTVLTREDGLKYYRMMQTVRRMELK	77
EGSDTVQIELPESSFESYMLEPPDLSYETSKATLLQMYKDMVIIRRMEMA	97
RLASTEATFQTCKPFKLHKLDGPDINVHVTKEDAVHYYTQMLTIRRMESA	73
GKFDPLKNEKVCVLDKDGVINPKLMPKISDQEILEAYKIMNLSRRQDIY	54
EKVAEQFPTFQILNEEGEVVNEEAMPELSDEQLKE-LMRRMVYTRILDQR	63
.....L.Y.M.RR.E..	100

o

CAQMYYRGKMFVHLYNGQEA VSTGFIKLLTKSDSVVSTYRDHVHALSK	150
CAQMYYKGKMFVHLYNGQEA VSTGVIKLLDSKDYVCSTYRDHVHALSK	90
ADSLYKANVIRGFCHLYDGQEAV AIGMEAAITKKDAIITAYRDHCIFLGR	125
ADQLYKQKIIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRAHGT FTR	127
CDALYKAKKIRGFCHLSVGQEAIAVGIENAITKLDIITSYRCHGFTFMR	147
AGNLYKEKKVRGFCHLYSGQEACAVGTTKAAMDAGDAAVTAYRCHGWTYLS	123
QNTMQRQGRLLSFLSSTGQEACEVAYINALNKTDHFVSGYRNNAAWLAM	104
SISLNQRQGRL-GFYAPTAGQEASQIA SHFALEKEDFILPGYRDVPQIIWH	112
...LY.....GF.HL..GQE A...G.....K.D.....YR.H.....	150

APPROVED BY DRAFTSMAN	O.G. FIG. CLASS SUBCLASS
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FIG. 8B

TPP-binding site

GVSARAVMSELFGKVITGCCRGQGGSMHMFSKEHNLGGFAFIGEGIPVAT	200
GVPSQNVMAELFGKETGCSRGRGGSMHIFSAPHNFLGGFAFIAEGIPVAT	140
GGSLHEVFSELMGRQAGCSKGKGGSMHFYKKESSFYGGHIVGAQVPLGC	175
GLSVREILAELTGRKGGCAKGKGGSMHMYAKN--FYGGNGIVGAQVPLGA	175
GASVRAVLAELMGRAGVSYGKGGSMHLYAPG--FYGGNGIVGAQVPLGA	195
GSSVAKVLCELTGRITGNVYKGKGGSMHMYGEN--FYGGNGIVGAQQPLGT	171
GQLVRNIMLYWIGNEAG-GKAPEG-VNCLPPN-----IVIGSQYSQAT	145
GLPLYQAFLFSRGHFHG-NQIPEG-VNVLPPQ-----IIIGAQYIQA	153

G.S...V..EL.G...G...G.GGSMH.....-F.GG..I.GAQ.P...	200
---	-----

PDH β binding site

GAAFSSKYRREVLKDQCD-DVTVAFFGDGTCNNGQFFECLNMAALYKLPI	249
GAASFQSIYRQQVLKEPGELRVTACFFGDGTTNNQFFECLNMAVLWKLPI	190
GIAFAQKYNKE---EA---VTFALYGDGAANQQLFEALNISALWDLPA	218
GIALACKYNGK---DE---VCLTLYGDGAANQGQIFEAYNMAALWKLPC	218
GLAFAHQYKNE---DA---CSFTLYGDGASNQGQVFESFMNAKLWNLPV	238
GIAFAMKYRKE---KN---VCITMFGDGATNQGQLFESMNMAKLWDLPV	214
GIAFADKYRKT---GG---VVVTTGDGGSSEGETYEAMNFAKLHEVPC	188
GVALGLKMRGK---KA---VAITYGDGGTSQGDFYEGINFAGAFKAPA	196

G.AFA.KYR.-----V..T..GDG..NQQQ.FE..NMA.LW.LP.	250
---	-----

*3

IFVVENNLWAIGMSHLRATSDPEIWKKPAFGMPGVHVDGMDVLKVREVA	299
IFVVENNQWAIGMAHHRSSSIPEIHKKAEAFGLPGIEVDGMDVLAVRQVA	240
ILVCENNHYGMGTAEWRAAKSPSYKRGD-Y-VPGLKVDGMDAFAVKQAC	266
IFICENNRGYMGTSVERAASTDYYKRGD-F-IPGLRVDGMDILCVREAT	266
VFCCEENNKGGMGTAASRSSAMTEYFKRGQ-Y-IPGLKVNMDILAVYQAS	286
LYVCENNGYGMGTAARSSASTDYYTRGD-Y-VPGIWVDGMDVLAVRQAV	262
IFVIENNWKWAISTARSEQTKSINFAVKGIAKGIPSIIIVDGNDYLACIGVF	238
IFVVQNNRFAISTPVEKQTVAKTLAQKAVAAGIPGIQVDGMDPLAVYAAV	246

IFV.ENN....GTA..R.....K.G....PG..VDGMD.LAV..A.	300
--	-----

*1 .2

KEAVTRARRGEGPTLVECETYRFRGHSLADPD-ELRDAAE-KAKYAARDP	347
EKAVERARQGQGPTLIEALTYRFRGHSLADPD-ELRSRQE-KEAWVARDP	288
KFAKQHCALE-KGPIILEMDTYRHYGHMSDPGSTYRTRDEISGVRQERDP	315
RFAAAAYCRSGKGPIILMELQTYRHYGHMSDPGVSYRTREEIQEVRSKSDP	316
KFAKDWDCLSGKGKGPLVLEYETYRYGGHMSDPGTTYRTRDEIQHMRSKNDP	336
RWAKEWCNAGKGPLMIEMATTYRYSGHMSDPGTSYRTREEQEVRKTRDP	312
KEVVEYVRKGNGPVLVECDTYRLGAHSSSDNPDAYRPKGEEFEM-AKFDP	287
KAARERAINGEGPTLIETLCFRYGPHTMSGDDPTRYRSKELENEWAKD	296

K.A.....G.GP.L.E..TYRY.GHMSDP...YR.R.E.....DP	350
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APPROVED BY DRAFTSMAN	O.G. FIG. CLASS	SUBCLASS
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FIG. 8C

IAALKKYLIENKLAKEAELKSIEKKIDELVEEAVEFADASPQPG--RSQL	395
IKKLKKHILDNQIASSDELNDIQSSVKIDLEQSVEFAMSSPEPN--ISEL	336
IERIKKLVLSHDLATEKELKDMEKEIRKEVDDAIAKAKDCPMPE--PSEL	363
IMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP--LEEL	364
IAGLKMHLLIDLGIAAEVAKYDKSARKYVDEQVELADAAPPPEAKLSIL	386
ITGFKDKIVTAGLVTEDEIKEIDKQVRKEIDAQVKAHTDKESPVELMLT	362
LIRLKQYLIDKKIWSDEQQAQLEAEQDKFVADEFAWVEKNKNYDL-IDIF	336
LVRFRKFLEAKGLWSEEEENNVIEQAKEEIKEAIKKADETPKQK--VTDL	344
I..LK.....LA.E.E.K.....K....A...A...P.P.----L	400

LENVFADPKGFGIGPDGRYRCEDPKFTEG-TAQV	428
-----K-----RY-----LFADN-----	344
FTNVYV--KGFG---TESFGPDRKEVKAS-LP--	389
GYHIYSSDPPF---EVRGANQWIKFKSVS----	390
FEDVYVKGTETPTLRGRIPEDTWDFKKQGFASRD	420
DIYYNTPAQYVRCTTDEVLQKYLTSEEAVKALAK	396
KYQYDKMDIFLEEQYKEAKEEFFEKYPESKEGGHH	370
ISIMFE-ELPF-----NLKEQYEIYKEKESK--	369
.....	434

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 9A

Plastid A.t.	MSSIIHGAGAATTLSTFNSVDSKKLFVAPSRTNLSVRSQLYIVAGSDAS	50
P.purpurea		
A.thaliana		
H.sapiens		
S.cerevisiae		
A.suum		MFS 3
M.capricolum		
B.subtilis		

Consensus		50
-----------	--	----

KKSFGSGLRVRHSQKLIPNAVATKEADTSASTGHELLLFEALQEGLEEM	100
-----MSKVFMFDALRAATDEEM	
MLGILRQRAIDGASTLRRTRFALVSARSYAAAGAKEMTVRDALNSAIDEEM	18
---MAAVSGLVRRPLREVSGLLKRRFHWTAPAALQVTVRDAINQGMDEEL	50
RLPTSLARNVARAPTSFVRPSAAAALRFSSTKTMVREALNSAMAEL	47
--MAVNGCMRLLRNGLTSACALEQSVRRLASGTLNVTVRDALNAALDEEI	53
-----MAIINNIKAVTDALDCAM	48
-----MAQMTMVQAITDALRIEL	18
-----T...AL..A.DEE.	100

Region 1

DRDPHVCMGEDVGHYGGSYKVTKGLADKFGDLRVLDTPICENAFTGMGI	150
EKDLTVCVIGEDVGHYGGSYKVTKDLHSKYGDLRVLDTPIAENSFTGMAI	68
SADPKVFMGEVGQYQGAYKITKGLLEKYGPERVYDTPITEAGFTGIGV	100
ERDEKVFLIGEEVAQYDGAYKVSRLWKKYGDRIIDTPISEMGFAGIAV	97
DRDDDVFLIGEEVAQYNGAYKVSKGLLDRFGERRVVDTPILEYGFTGLAV	103
KRDDDRVFLIGEEVAQYDGAYKISKGLWKKYGDRIWDTPITEMAIAGLSV	98
QRDPNVIVFGEDVGTEGGVFRATQGLAVKFGNDRCFNAPISEAMFAGVGL	68
KNDPNVLIFGEDVGVNGGVFRATEGLQAEFGEDRVFDTPLAESGIGGLAI	68
.RD..V...GE.VG.Y.G.YK.TKGL..K.G..RV.DTPI.E..F.G...	150

GAAMTGLRPVIEGMNMGFLLAfnQISNNCGMLHYTSGQFTIPVVIIRGP	200
GAAITGLRPIVEGMNMSFLLAfnQISNNAGMLRYTSGGNFTLPLVIRGP	118
GAAYAGLKPVEFMTFNSMQAIDHIINSAAKSNYMSAGQINVPIVFRGP	150
GAAMAGLRPICEFMTFNSMQAIDQVINSAAKTYYMSGGLQPVPIVFRGP	147
GAALKGLKPIVEFMSFNFSMQAIDHVVNSAAKTHYMSGGTQKCQMVFRGP	153

APPROVED BY DRAFTSMAN	O.G. FIG. CLASS SUBCLASS
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FIG. 9B

GAAMNGLRPICEFMSMNFSMQGIDHIINSAAKAHYMSAGRHFHVPIVFRGA	148
GMAMNGMKPVLEMQFEGLGLASLQNIFTNISRMNRTRGKYTAPMIVRMP	118
GLALQGFRPVPEIQFFGFVYEVMDSCIGQMARIRYRTGGRYHMPITIRSP	118
GAA..GLRP..E.M...F...A.D.I.N.AA...Y.SGG....P.V.RGP	200

Region 2

GGVGRQLGAEHSQRLESYFQSIPGIQMVA CSTPYN A KGLMKA AIRSEN PV	250
GGVGRQLGAEHSQRLEAYFQAIPGLKIVACSTPYN A KGLMKA AIRDNN PV	168
NGAAAGVGAQHSQCYAAWYASVPGKLVAPYSAEDARGLLKAAIRDPDPV	200
NGASAGVAAQHSQCFAAWYGHCPGLKVVSPWNSEDAKGLIKSAIRDNN PV	197
NGAAVGLGAQHSQDFSPWYGSIPGLKVLV P YSAEDARGLLKAAIRDPNPV	203
NGAAVGVAQQHSQDFTAWFMHCPGVKVVV PYD CEDARGLLKAAVRDDNPV	198
MGGGIRALEHHSEALEAVYAHIPGVQIVCPSTPYDTKGLLIAIDSPDPV	168
FGGGVHTPELHSDSLEGLVAQQPGLKVVIPSTPYDAKGLLISAIRDNDPV	168
.G.....A.HSQA.....A.....PGLKVV.P.....DAKGLLKAIRD.NPV	250

ILFEHVLLYN---LKEKIPDEDYICNLEEAEMVRPGEHITILTYSRMRY	296
VFFEHVLLYN---LQEEIPEDEYLIPLDKAEVVVRKGKDITILTYSRMRH	214
VFLENELLYGESFPISSEEALDSSFC LPIGAKIEREGKDVTIVTFSKMVG	250
VFLENELLYGVPF EFLPEAQSKDFLPIGAKIERQGTHITVVSHSRPVG	247
VFLENELLYGESFEIISSEEALSPFETLPY-KAKIEREGTDISIVTYTRNVQ	252
ICLENEILYGMKFPVSPEAQSPDFVLPFGQAKIQRPGKDITIVSLSIGVD	248
IVVEPTKLYR---AFKQEV PDEHYIVPIGEGYKIQEGNDLTVVTVGAQTV	215
IFLEHLKLYR---SFRQEVPEGEYTIPIGKADIKREGKDITIIAYGAMVH	215
.LE..LLY.....E.....P.GKA.I.R.G.DITIVTYS..V.	300

Region 3

HVMQAAKTLVNK--GYDPEVIDIRSLKPFDLHTIGNSVKKTHRVLIVEEC	344
HVTEALPLLLND--GYDPEVLDLISLKPLDIDSISVSVKKTHRVLIVEEC	262
FALKAAEKLAAE--GISAEVINLRSIRPLDRATINASVRKTSRLVTVEEG	298
HCLEAAAVLSKE--GVECEVINMRTI RPMDMETIEASVMKTNHLVTVEGG	295
FSLEAAEILQKKY-GVSAEVINLRSIRPLDTEAIIKTVKKTNHLITVEST	301
VSLHAADELAKS--GIDCEVINLRCVRPLDFQTVKDSVIKTKHLVTVESG	296
DCQKAIALLKETHPNATIDLIDLRSIKPWDKKMVI E SVKKTGRLLVVHEA	265
ESLKAAAEELEKE--GISAEVVDLRTVQPLDIETIIGSVEKTGRAIVVQEA	263
.L.AA..L....-G...EVI.LRS..PLD..TI..SV.KT.RL..VEE.	350

Region 4

MRTGGIGASLTA AINE-NFH DYLDAPVMCLSSQDVPTPYAGTLEEWTVVQ	393
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APPROVED BY DRAFTSMAN	O.G. FIG. CLASS SUBCLASS
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FIG. 9C

MKTAGIGAELIAQINE-HLFDELDAPVVRLLSSQDIPTPYNGSLEQATVIQ	311
FPQHGVCACAEICASVVE-ESFSYLDAPVERIAGADVPIPYTANLERLALPQ	347
WPQFGVGAEICARIMEGPAFNFLDAPAVRVTGADVPMPYAKILEDNSIPQ	345
FPSFGVGAEIVAQVMESEAFDYLDAPIQRVTGADVPTPYAKELEDFAFPD	351
WPNCVGVAEISARVTESDAFGYLDGPILRVTGVDVPMPYAQPLETAALPQ	346
VKSFSVSAEIIATVNE-ECFEYIKAPLSRCTGYDVITPDFDRG-EGYFQVN	313
QRQAGIAANVVAEINE-RAILSLEAPVLRVAAPDTVYPFAQA-ESVWLPN	311
....GVGAEI.A...E-..F.YLDAP..R..G.DVP.PY...LE....PQ	400
PAQIVTAVEQLCQ-----	406
PHQIIDAVKNIVNSSKTITT	331
IEDIVRASKRACYRSK---	363
VKDIIFAIKKTLNI-----	359
TPTIVKAVKEVLSIE-----	366
PADVVKMVKKCLNVQ-----	361
PKKVLVKMQUELLDFKF---	329
FKDVIETAKKVMNF-----	325
...I..A.K.....-----	420

APPROVED	O. G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

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FIG: 10A

A. t.	MAA-----LLG-RSC-----RKLSFPSLTHG-----ARR- 23
Human	MAVVAAAAGWLLRLRAAGAEGHWRRRLPGAGLARGFLHPAATVEDAAQRRQ 50
Bovine	MAAAVAAFAGWLLRLRAAGADGPWRRLCGAGLSRGFLQSASAY-GAAQRRQ 49
Consensus	MAAVAA . AGWLLRLRAAGA . G . WRRL . GAGL . RGFL . A AAQRRQ 50

V-----STETGKP--LNLYSAINQALHIALDTPRSYVFGEDVGF	61
VAHFTQPDPEPREYGQTQKMLFQSVTSDLNSLAKDPTAVIFGEDVAF	100
VAHFTQPDPEPVEYGQTQKMLFQAVTSALDNSLAKDPTAVIFGEDVAF	99
VAHFTQPDPEP . EYGQTQKMLFQAVTSALDNSLAKDPTAVIFGEDVAF	100

GGVFRCTTGLAERFGKNRVFNTPLCEQGIVGFGIGLAAMGNRAIVEIQFA	111
GGVFRCTVGLRDKYKGKDRVFTPLCEQGIVGFGIGIAVTGATAIAEIQFA	150
GGVFRCTVGLRDKYKGKDRVFTPLCEQGIVGFGIGIAVTGATAIAEIQFA	149
GGVFRCTVGLRDKYKGKDRVFTPLCEQGIVGFGIGIAVTGATAIAEIQFA	150

DYIYPAFDQIVNEAAKFRYRSGNQFNCGGLTIRAPYGAVGHGGHYHSQSP	161
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	200
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	199
DYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSP	200

EAFFCHVPGIKVVI PRSPREAKGLLSCIRDNPVVFFEPKWLYRQAVEE	211
EAFFAHCPGIKVVI PRSPFQAKGLLSCIEDKNPCIFFEPKILYRAAEE	250
EAFFAHCPGIKVVI PRSPFQAKGLLSCIEDKNPCIFFEPKILYRAAVEQ	249
EAFFAHCPGIKVVI PRSPFQAKGLLSCIEDKNPCIFFEPKILYRAAVEE	250

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

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FIG. 10B

VPEHDYMIPLSEAEVIREGNDITLVGWAQLTVMEQ-ACLDAEKEGISCE	260
VPIEPYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSC	300
VPVEPYNIPLSQAEVIQEGSDVTLVAWGTQVHEIREVAAMAQEKLGVSC	299
VP.EPYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVA.MA.EKLGVSC	300
LIDLKTLLPWDKETVEASVKKTGRLLISHEAPVTGGFGAEISATILERCF	310
VIDLRTIIPWDVDTICKSVIKSGRLLISHEAPLTGGFASEISSTVQEECF	350
VIDLRTILPWDVDTVCKSVIKTGRLLVSHEAPLTGGFASEISSTVQEQQCF	349
VIDLRTILPWDVDTVCKSVIKTGRLLISHEAPLTGGFASEISSTVQE.CF	350
LKLEAPVSRVCGLDTPFPLVFEPEFYMPYKNKILDIAIKSTVNY	352
LNLEAPISRVCGYDTPFPFHIFEPFYIPDKWKCYDALRKMINY	392
LNLEAPISRVCGYDTPFPFHIFEPFYIPDKWKCYDALRKMINY	391
LNLEAPISRVCGYDTPFPFHIFEPFYIPDKWKCYDALRKMINY	392